

EXHIBIT 6

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Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

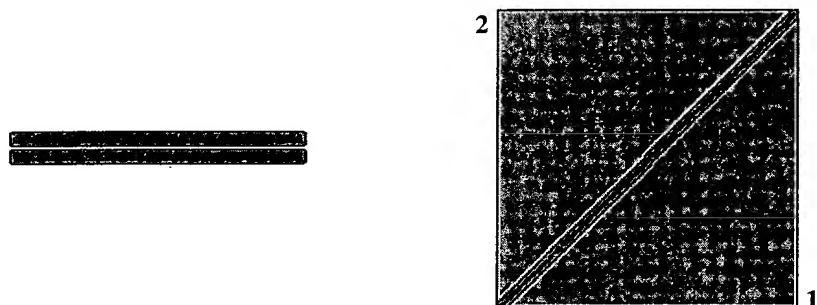
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.15 [Oct-15-2006]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0000** wordsize: **3** Filter ☐ View option **Standard**
 Masking character option **X for protein, n for nucleotide** Masking color option **Black**
☐ Show CDS translation **Align**

Sequence 1: gi|6678678|ref|NP_032519.1|leptin [Mus musculus] >gi|730219|sp|P41160|LEP_MOUSE Leptin precursor (Obesity factor) >gi|603288|gb|AAA64564.1| ob >gi|726297|gb|AAA64213.1| obesity protein >gi|26326917|dbj|BAC27202.1| unnamed protein product [Mus musculus] >gi|74216350|dbj|BAE25117.1| unnamed protein product [Mus musculus] >gi|115545388|gb|AAI25246.1| Leptin [Mus musculus] >gi|1092655|prf|2024338A obeser gene Length = 167 (1 .. 167)

Sequence 2: gi|6981148|ref|NP_037208.1|leptin [Rattus norvegicus] >gi|1709436|sp|P50596|LEP_RAT Leptin precursor (Obesity factor) >gi|2144095|pir|I55622 rat ob - rat >gi|995615|dbj|BAA08529.1| leptin (ob product) [Rattus norvegicus] >gi|1018991|dbj|BAA08296.1| rat ob [Rattus sp.] >gi|9800646|gb|AAB34657.2| obese [Rattus norvegicus] Length = 167 (1 .. 167)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 322 bits (825), Expect = 6e-87
 Identities = 161/167 (96%), Positives = 165/167 (98%), Gaps = 0/167 (0%)

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Identities = 161/167 (96%), Positives = 165/167 (98%), Gaps = 0/167 (0%)

Query 1 MCWRPLCRFLWLWSYLSYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSAKQRVVTGL 60
      MCWRPLCRFLWLWSYLSYVQAVPI KVQDDTKTLIKTIVTRINDISHTQSVSA+QRVVTGL
Sbjct 1 MCWRPLCRFLWLWSYLSYVQAVPIHKVQDDTKTLIKTIVTRINDISHTQSVSARQRVVTGL 60

Query 61 DFIPGLHPILSLSKMDQTLAVYQQVLTSLPSQNVLQIANDLENLRDLLHLLAFSKSCSLP 120
      DFIPGLHPILSLSKMDQTLAVYQQ+LTSLPSQNVLQIA+DLENLRDLLHLLAFSKSCSLP
Sbjct 61 DFIPGLHPILSLSKMDQTLAVYQQILTSLPSQNVLQIAHDLENLRDLLHLLAFSKSCSLP 120

Query 121 QTSGLQKPESLDGVLEASLYSTEVALSRLQGSQDILQQQLDVSPEC 167
      QT GLQKPESLDGVLEASLYSTEVALSRLQGSQDILQQQLD+SPEC
Sbjct 121 QTRGLQKPESLDGVLEASLYSTEVALSRLQGSQDILQQQLDLSPEC 167
  
```

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

| Lambda | K | H |
|--------|-------|-------|
| 0.319 | 0.133 | 0.387 |

Gapped

| Lambda | K | H |
|--------|--------|-------|
| 0.267 | 0.0410 | 0.140 |

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 324

Number of extensions: 121

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 167

Length of database: 1,565,033,500

Length adjustment: 124

Effective length of query: 43

Effective length of database: 1,565,033,376

Effective search space: 67296435168

Effective search space used: 67296435168

Neighboring words threshold: 9

X1: 16 (7.4 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.8 bits)

S2: 73 (32.7 bits)